

200

1cm8\_P38g  
1jwh\_CK2a  
1fvv\_CDk2  
13929114.m  
6754200.m  
HIPK3.h  
HIPK2.h  
6754198.m  
34855173.m  
6754196.m  
HIPK1.h  
34860081.m  
25146830.w  
25146832.w  
25146827.w  
24654777.f  
24654780.f  
31199043.i  
27676686.m  
38086162.m  
HIPK4.h  
AK100925.q  
AK066639.q  
15239248.p  
19114742.y  
6322320.y  
1how\_Ymr21

400

1cm8\_P38g  
1jwh\_CK2a  
1fvv\_CDk2  
13929114.m  
6754200.m  
HIPK3.h  
HIPK2.h  
6754198.m  
34855173.m  
6754196.m  
HIPK1.h  
34860081.m  
25146830.w  
25146832.w  
25146827.w  
24654777.f  
24654780.f  
31199043.i  
27676686.m  
38086162.m  
HIPK4.h  
AK100925.q  
AK066639.q  
15239248.p  
19114742.y  
6322320.y  
1how\_Ymr21

Sequence alignment showing conservation across various proteins. The alignment spans from position 400 to 590 and 610 to 790. The y-axis lists protein names and their IDs. A color key indicates conservation levels: black (most conserved), red, green, blue, magenta, cyan, yellow, and orange (least conserved).

**Top Alignment (Positions 400-590):**

- lcm8\_P38g: VAIKLKNP~~S~~YARQGQIEVSILRLS
- 1jwh\_CK2a: VVWKLKP~~C~~EGKKKKRKEIKLE
- 1fvv\_CDK2: VALKKR~~T~~DTEGVPSAIRETSLK
- 13929114.m: VAIIKLN~~N~~P~~S~~YARQGQIEVSILRLS
- 6754200.m: VAIIKLN~~N~~P~~S~~YARQGQIEVSILRLS
- HIPK3.h: VAIIKLN~~N~~P~~S~~YARQGQIEVSILRLS
- HIPK2.h: VAIIKLN~~N~~P~~S~~YARQGQIEVSILRLS
- 6754198.m: VAIIKLN~~N~~P~~S~~YARQGQIEVSILRLS
- 34855173.m: VAIIKLN~~N~~P~~S~~YARQGQIEVSILRLS
- 6754196.m: VAIIKLN~~N~~P~~S~~YARQGQIEVSILRLS
- HIPK1.h: VAIIKLN~~N~~P~~S~~YARQGQIEVSILRLS
- 34860081.m: VAIIKLN~~N~~P~~S~~YARQGQIEVSILRLS
- 25146830.w: VAIIKLN~~K~~P~~S~~YARQGQIEVSILRLS
- 25146832.w: VAIIKLN~~K~~P~~S~~YARQGQIEVSILRLS
- 25146827.w: VAIIKLN~~K~~P~~S~~YARQGQIEVSILRLS
- 24654777.f: VAIIKLN~~N~~P~~S~~YARQGQIEVSILRLS
- 24654780.f: VAIIKLN~~N~~P~~S~~YARQGQIEVSILRLS
- 31199043.i: VAIIKLN~~N~~P~~S~~YARQGQIEVSILRLS
- 27676688.m: VAIIKLN~~D~~A~~V~~RSRIKNEELKLRLCVR
- AK066639.q: VAIIKLN~~D~~A~~V~~RSRIKNEELKLRLCVR
- 15239248.p: VAIIKLN~~D~~A~~V~~RSRIKNEELKLRLCVR
- 19114742.y: VAIIKLN~~D~~A~~V~~RSRIKNEELKLRLCVR
- 6322320.y: LAVKVK~~R~~SE~~T~~LT~~S~~SI~~E~~AN~~L~~PL~~N~~RA~~N~~Q~~T~~
- 1how\_Ymr21: VAMKIV~~R~~SDKV~~M~~TEAAE~~C~~I~~K~~LR~~N~~DA~~D~~NT~~K~~DD~~S~~MC~~A~~HL~~I~~KL~~D~~PF~~H~~KG~~N~~GV~~H~~VVM~~V~~FEVL~~G~~EN~~I~~AI~~K~~Y~~E~~HRG

**Bottom Alignment (Positions 610-790):**

- lcm8\_P38g: CIMAEM~~T~~~~C~~KLF~~C~~
- 1jwh\_CK2a: CMIA~~M~~IFRK~~C~~FFF~~C~~
- 1fvv\_CDK2: C~~I~~FAEM~~V~~TR-RALF~~C~~
- 13929114.m: CVIAELFLG~~M~~WLY~~C~~
- 6754200.m: CVIAELFLG~~M~~WLY~~C~~
- HIPK3.h: CVIAELFLG~~M~~WLY~~C~~
- HIPK2.h: CVIAELFLG~~M~~WLY~~C~~
- 6754198.m: CVIAELFLG~~M~~WLY~~C~~
- 34855173.m: CVIAELFLG~~M~~WLY~~C~~
- 6754196.m: CVIAELFLG~~M~~WLY~~C~~
- HIPK1.h: CVIAELFLG~~M~~WLY~~C~~
- 34860081.m: CVIAELFLG~~M~~WLY~~C~~
- 25146830.w: CVIAELFLG~~M~~WLY~~C~~
- 25146832.w: CVIAELFLG~~M~~WLY~~C~~
- 25146827.w: CVIAELFLG~~M~~WLY~~C~~
- 24654777.f: CVIAELFLG~~M~~WLY~~C~~
- 24654780.f: CVIAELFLG~~M~~WLY~~C~~
- 31199043.i: CVIAELFLG~~M~~WLY~~C~~
- 27676688.m: CVIAELFLG~~M~~WLY~~C~~
- AK066639.q: CVIAELFLG~~M~~WLY~~C~~
- 15239248.p: CVIAELFLG~~M~~WLY~~C~~
- 19114742.y: CVIAELFLG~~M~~WLY~~C~~
- 6322320.y: CVIAELFLG~~M~~WLY~~C~~
- 1how\_Ymr21: CVIAELFLG~~M~~WLY~~C~~

1cm8\_P38g VLSFKPPRQLGARVSKETPL  
 1jwh\_CK2a  
 1fvv\_CDK2  
 13929114.m SK--MSLRPVAASNGTAALAANFTKVGT-  
 6754200.m SK--MSLRPVAASNGTAALAANFTKVGT-  
 HIPK3.h NK--TSLRPPVASSSTATLTANFTIKIGT-  
 HIPK2.h SK--TPFVTHVAPSTNSTLMTFNNQLT-  
 6754198.m SK--TPFVTHVAPSTNSTLMTFNNQLT-  
 34855173.m SK--TPFVTHVAPSTNSTLMTFNNQLT-  
 6754196.m IX--SPFVTHVAPNTNSTLMSFSNQLN-  
 HIPK1.h IX--SPFVTHVAPNTNSTLMSFSNQLN-  
 3486081.m IX--SPFVTHVAPNTNSTLMSFSNQLN-  
 25146830.w AANVATP<sup>T</sup>TPVEKPPAPKLQQPMIAVLP-  
 25146832.w AANVATP<sup>T</sup>TPVEKPPAPKLQQPMIAVLP-  
 25146827.w AANVATP<sup>T</sup>TPVEKPPAPKLQQPMIAVLP-  
 24654777.f ASTLVNFVPSSTENMTFTINNQLT-  
 24654780.f ASTLVNFVPSSTENMTFTINNQLT-  
 31199043.i T-TATLWTFNVPNTTENMTTTFNN-  
 27676688.m KP--PPPVLANAEADGPPYYRLAEEETAG-  
 38088162.m KP--PPPVLASAAEDGPPYYRLAEEETAG-  
 HIPK4.h KP--PTPVWA AEDGTPYYCLAEKEEAAG-  
 AK100925.q AAAGLSPQGSVNRSLPPNNPYPKIPYSH-  
 AK066639.q AAAGLSPQGSSTINRGLPFNNAPAKLPPFSG-  
 15239248.p AAAGLSPHPSGRURIDMHNSPHFQMPMYSH-  
 19114742.y TRNRSHTCQNQAVVPPS-  
 6322320.y ANDSSNNAGHNYVYNPSSATGGADSDVIG-  
 1how\_Ymr21



